



SEQUENCE LISTING

<110> The Regents of the University of California
 Shi, Huazhong
 Blumwald, Eduardo

<120> IMPROVED TRANSPORTERS AND THEIR USES

<130> 023070-127310US

<140> US 10/520,497

<141> 2003-07-09

<150> WO PCT/US2003/021549

<151> 2003-07-09

<150> US 60/395,662

<151> 2002-07-12

<160> 22

<170> PatentIn version 3.3

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<211> 1614

<212> DNA

<213> Arabidopsis thaliana

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cataccttgc caactttgtc atttcttgcg gagacatttgc ttgttgc ttgttggatg		960

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<212> PRT
<213> *Arabidopsis thaliana*

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20 25 30

Cys Ile Val Leu Gly His Leu Leu Glu Glu Asn Arg Trp Met Asn Glu
35 40 45

Ser Ile Thr Ala Leu Leu Ile Gly Leu Gly Thr Gly Val Thr Ile Leu
50 55 60

Leu Ile Ser Lys Gly Lys Ser Ser His Leu Leu Val Phe Ser Glu Asp
65 70 75 80

Leu Phe Phe Ile Tyr Leu Leu Pro Pro Ile Ile Phe Asn Ala Gly Phe
85 90 95

Gln Val Lys Lys Lys Gln Phe Phe Arg Asn Phe Val Thr Ile Met Leu
100 105 110

Phe Gly Ala Val Gly Thr Ile Ile Ser Cys Thr Ile Ile Ser Leu Gly
115 120 125

Val Thr Gln Phe Phe Lys Lys Leu Asp Ile Gly Thr Phe Asp Leu Gly
130 135 140

Asp Tyr Leu Ala Ile Gly Ala Ile Phe Ala Ala Thr Asp Ser Val Cys
145 150 155 160

Thr Leu Gln Val Leu Asn Gln Asp Glu Thr Pro Leu Leu Tyr Ser Leu
165 170 175

Val Phe Gly Glu Gly Val Val Asn Asp Ala Thr Ser Val Val Val Phe
180 185 190

Asn Ala Ile Gln Ser Phe Asp Leu Thr His Leu Asn His Glu Ala Ala
195 200 205

Phe His Leu Leu Gly Asn Phe Leu Tyr Leu Phe Leu Leu Ser Thr Leu
210 215 220

Leu Gly Ala Ala Thr Gly Leu Ile Ser Ala Tyr Val Ile Lys Lys Leu
225 230 235 240

Tyr Phe Gly Arg His Ser Thr Asp Arg Glu Val Ala Leu Met Met Leu
245 250 255

Met Ala Tyr Leu Ser Tyr Met Leu Ala Glu Leu Phe Asp Leu Ser Gly
260 265 270

Ile Leu Thr Val Phe Phe Cys Gly Ile Val Met Ser His Tyr Thr Trp
275 280 285

His Asn Val Thr Glu Ser Ser Arg Ile Thr Thr Lys His Thr Phe Ala
290 295 300

Thr Leu Ser Phe Leu Ala Glu Thr Phe Ile Phe Leu Tyr Val Gly Met
305 310 315 320

Asp Ala Leu Asp Ile Asp Lys Trp Arg Ser Val Ser Asp Thr Pro Gly
325 330 335

Thr Ser Ile Ala Val Ser Ser Ile Leu Met Gly Leu Val Met Val Gly
340 345 350

Arg Ala Ala Phe Val Phe Pro Leu Ser Phe Leu Ser Asn Leu Ala Lys
355 360 365

Lys Asn Gln Ser Glu Lys Ile Asn Phe Asn Met Gln Val Val Ile Trp
370 375 380

Trp Ser Gly Leu Met Arg Gly Ala Val Ser Met Ala Leu Ala Tyr Asn
385 390 395 400

Lys Phe Thr Arg Ala Gly His Thr Asp Val Arg Gly Asn Ala Ile Met
405 410 415

Ile Thr Ser Thr Ile Thr Val Cys Leu Phe Ser Thr Val Val Phe Gly
420 425 430

Met Leu Thr Lys Pro Leu Ile Ser Tyr Leu Leu Pro His Gln Asn Ala
435 440 445

Thr Thr Ser Met Leu Ser Asp Asp Asn Thr Pro Lys Ser Ile His Ile
450 455 460

Pro Leu Leu Asp Gln Asp Ser Phe Ile Glu Pro Ser Gly Asn His Asn
465 470 475 480

Val Pro Arg Pro Asp Ser Ile Arg Gly Phe Leu Thr Arg Pro Thr Arg
485 490 495

Thr Val His Tyr Tyr Trp Arg Gln Phe Asp Asp Ser Phe Met Arg Pro
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Val Phe Gly Gly Arg Gly Phe Val Pro Phe Val Pro Gly Ser Pro Thr
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Glu Arg Asn Pro Pro Asp Leu Ser Lys Ala
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gaagagaata gatggatgaa cgaatccatc accgccttgt tgattggct aggcactggt 180
gttaccattt tggatttag taaaggaaaa agctcgcatac ttctcgtctt tagtgaagat 240

cttttcttca tataatctttt	300
gccaccatt atattcaatg	
cagggtttca agtaaaaaaag	
aaggcgtttt tccgcaattt	360
cgtgactatt atgcttttg	
gtgctgttgg gactattatt	
tcttgcacaa tcataatctct	420
aggtgtaca cagttcttta	
agaagttgga cattggAAC	
tttgacttgg gtgattatct	480
tgctatttgtt gccatatttgc	
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acactgcagg ttctgaatca	540
agacgagaca ccttgctt	
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ggtgttgtga atgatgcaac	600
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cgattcagag ctttgatctc	
actcacctaa accacgaagc	660
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cgtatgttat caagaagcta	
tactttggaa ggcactcaac	780
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caccggAAC atcgatcgca	
gtgagctcaa tcctaattggg	1080
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cagcggtcgctt cttccgtt	
tcgtttctat ctaacttagc	1140
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aaatcaactt taacatgcag	
gttggattt ggtggcttgg	1200
tctcatgaga ggtgctgtat	
ctatggctct tgcatacaac	
aagtttacaa gggccgggca	1260
cacagatgta cgcgggaaatg	
caatcatgat cacgagtacg	
ataactgtct gtcttttag	1320
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tgaccaaacc actcataagc	
tacctattac cgccaccagaa	1380
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ctgatgacaa caccggaaaa	
tccatacata tccctttgtt	1440
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gtgcctcggc ctgacagtat	1500
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ccactcgaac cgtgcattac	
tactggagac aatttcatg	1560
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ttggaggtcg tggctttgtt	
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 <213> Artificial

<220>
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20 25 30

Cys Ile Val Leu Gly His Leu Leu Glu Glu Asn Arg Trp Met Asn Glu
35 40 45

Ser Ile Thr Ala Leu Leu Ile Gly Leu Gly Thr Gly Val Thr Ile Leu
50 55 60

Leu Ile Ser Lys Gly Lys Ser Ser His Leu Leu Val Phe Ser Glu Asp
65 70 75 80

Leu Phe Phe Ile Tyr Leu Leu Pro Pro Ile Ile Phe Asn Ala Gly Phe
85 90 95

Gln Val Lys Lys Lys Gln Phe Phe Arg Asn Phe Val Thr Ile Met Leu
100 105 110

Phe Gly Ala Val Gly Thr Ile Ile Ser Cys Thr Ile Ile Ser Leu Gly
115 120 125

Val Thr Gln Phe Phe Lys Lys Leu Asp Ile Gly Thr Phe Asp Leu Gly
130 135 140

Asp Tyr Leu Ala Ile Gly Ala Ile Phe Ala Ala Thr Asp Ser Val Cys
145 150 155 160

Thr Leu Gln Val Leu Asn Gln Asp Glu Thr Pro Leu Leu Tyr Ser Leu
165 170 175

Val Phe Gly Glu Gly Val Val Asn Asp Ala Thr Ser Val Val Val Phe
180 185 190

Asn Ala Ile Gln Ser Phe Asp Leu Thr His Leu Asn His Glu Ala Ala
195 200 205

Phe His Leu Leu Gly Asn Phe Leu Tyr Leu Phe Leu Leu Ser Thr Leu
210 215 220

Leu Gly Ala Ala Thr Gly Leu Ile Ser Ala Tyr Val Ile Lys Lys Leu
225 230 235 240

Tyr Phe Gly Arg His Ser Thr Asp Arg Glu Val Ala Leu Met Met Leu
245 250 255

Met Ala Tyr Leu Ser Tyr Met Leu Ala Glu Leu Phe Asp Leu Ser Gly

260

265

270

Ile Leu Thr Val Phe Phe Cys Gly Ile Val Met Ser His Tyr Thr Trp
275 280 285

His Asn Val Thr Glu Ser Ser Arg Ile Thr Thr Lys His Thr Phe Ala
290 295 300

Thr Leu Ser Phe Leu Ala Glu Thr Phe Ile Phe Leu Tyr Val Gly Met
305 310 315 320

Asp Ala Leu Asp Ile Asp Lys Trp Arg Ser Val Ser Asp Thr Pro Gly
325 330 335

Thr Ser Ile Ala Val Ser Ser Ile Leu Met Gly Leu Val Met Val Gly
340 345 350

Arg Ala Ala Phe Val Phe Pro Leu Ser Phe Leu Ser Asn Leu Ala Lys
355 360 365

Lys Asn Gln Ser Glu Lys Ile Asn Phe Asn Met Gln Val Val Ile Trp
370 375 380

Trp Ser Gly Leu Met Arg Gly Ala Val Ser Met Ala Leu Ala Tyr Asn
385 390 395 400

Lys Phe Thr Arg Ala Gly His Thr Asp Val Arg Gly Asn Ala Ile Met
405 410 415

Ile Thr Ser Thr Ile Thr Val Cys Leu Phe Ser Thr Val Val Phe Gly
420 425 430

Met Leu Thr Lys Pro Leu Ile Ser Tyr Leu Leu Pro His Gln Asn Ala
435 440 445

Thr Thr Ser Met Leu Ser Asp Asp Asn Thr Pro Lys Ser Ile His Ile
450 455 460

Pro Leu Leu Asp Gln Asp Ser Phe Ile Glu Pro Ser Gly Asn His Asn
465 470 475 480

Val Pro Arg Pro Asp Ser Ile Arg Gly Phe Leu Thr Arg Pro Thr Arg
485 490 495

Thr Val His Tyr Tyr Trp Arg Gln Phe Asp Asp Cys Phe Met Arg Pro
500 505 510

Val Phe Gly Gly Arg Gly Phe Val Pro Phe Val Pro Gly Ser Pro Thr
515 520 525

Glu Arg Asn Pro Pro Asp Leu Ser Lys Ala
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<213> Artificial

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20 25 30

Cys Ile Val Leu Gly His Leu Leu Glu Glu Asn Arg Trp Met Asn Glu
35 40 45

Ser Ile Thr Ala Leu Leu Ile Gly Leu Gly Thr Gly Val Thr Ile Leu
50 55 60

Leu Ile Ser Lys Gly Lys Ser Ser His Leu Leu Val Phe Ser Glu Asp
65 70 75 80

Leu Phe Phe Ile Tyr Leu Leu Pro Pro Ile Ile Phe Asn Ala Gly Phe
85 90 95

Gln Val Lys Lys Lys Gln Phe Phe Arg Asn Phe Val Thr Ile Met Leu
100 105 110

Phe Gly Ala Val Gly Thr Ile Ile Ser Cys Thr Ile Ile Ser Leu Gly
115 120 125

Val Thr Gln Phe Phe Lys Lys Leu Asp Ile Gly Thr Phe Asp Leu Gly
130 135 140

Asp Tyr Leu Ala Ile Gly Ala Ile Phe Ala Ala Thr Asp Ser Val Cys
145 150 155 160

Thr Leu Gln Val Leu Asn Gln Asp Glu Thr Pro Leu Leu Tyr Ser Leu
165 170 175

Val Phe Gly Glu Gly Val Val Asn Asp Ala Thr Ser Val Val Val Phe
180 185 190

Asn Ala Ile Gln Ser Phe Asp Leu Thr His Leu Asn His Glu Ala Ala
195 200 205

Phe His Leu Leu Gly Asn Phe Leu Tyr Leu Phe Leu Leu Ser Thr Leu
210 215 220

Leu Gly Ala Ala Thr Gly Leu Ile Ser Ala Tyr Val Ile Lys Lys Leu
225 230 235 240

Tyr Phe Gly Arg His Ser Thr Asp Arg Glu Val Ala Leu Met Met Leu
245 250 255

Met Ala Tyr Leu Ser Tyr Met Leu Ala Glu Leu Phe Asp Leu Ser Gly
260 265 270

Ile Leu Thr Val Phe Phe Cys Gly Ile Val Met Ser His Tyr Thr Trp
275 280 285

His Asn Val Thr Glu Ser Ser Arg Ile Thr Thr Lys His Thr Phe Ala
290 295 300

Thr Leu Ser Phe Leu Ala Glu Thr Phe Ile Phe Leu Tyr Val Gly Met
305 310 315 320

Asp Ala Leu Asp Ile Asp Lys Trp Arg Ser Val Ser Asp Thr Pro Gly
325 330 335

Thr Ser Ile Ala Val Ser Ser Ile Leu Met Gly Leu Val Met Val Gly
340 345 350

Arg Ala Ala Phe Val Phe Pro Leu Ser Phe Leu Ser Asn Leu Ala Lys
355 360 365

Lys Asn Gln Ser Glu Lys Ile Asn Phe Asn Met Gln Val Val Ile Trp
370 375 380

Trp Ser Gly Leu Met Arg Gly Ala Val Ser Met Ala Leu Ala Tyr Asn
385 390 395 400

Lys Phe Thr Arg Ala Gly His Thr Asp Val Arg Gly Asn Ala Ile Met
405 410 415

Ile Thr Ser Thr Ile Thr Val Cys Leu Phe Ser Thr Val Val Phe Gly
420 425 430

Met Leu Thr Lys Pro Leu Ile Ser Tyr Leu Leu Pro His Gln Asn Ala
435 440 445

Thr Thr Ser Met Leu Ser Asp Asp Asn Thr Pro Lys Ser Ile His Ile
450 455 460

Pro Leu Leu Asp Gln Asp Ser Phe Ile Glu Pro Ser Gly Asn His Asn
465 470 475 480

Val Pro Arg Pro Asp Ser Ile Arg Gly Phe Leu Thr Arg Pro Thr Arg
485 490 495

Thr Val His Tyr Tyr Trp Arg Gln Phe Asp Asp Ser Phe Met Arg Pro
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Val Phe Gly Gly Arg Gly Phe Val Pro
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<212> PRT
<213> Artificial

<220>
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<400> 8

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20 25 30

Cys Ile Val Leu Gly His Leu Leu Glu Glu Asn Arg Trp Met Asn Glu
35 40 45

Ser Ile Thr Ala Leu Leu Ile Gly Leu Gly Thr Gly Val Thr Ile Leu
50 55 60

Leu Ile Ser Lys Gly Lys Ser Ser His Leu Leu Val Phe Ser Glu Asp
65 70 75 80

Leu Phe Phe Ile Tyr Leu Leu Pro Pro Ile Ile Phe Asn Ala Gly Phe
85 90 95

Gln Val Lys Lys Lys Gln Phe Phe Arg Asn Phe Val Thr Ile Met Leu
100 105 110

Phe Gly Ala Val Gly Thr Ile Ile Ser Cys Thr Ile Ile Ser Leu Gly
115 120 125

Val Thr Gln Phe Phe Lys Lys Leu Asp Ile Gly Thr Phe Asp Leu Gly
130 135 140

Asp Tyr Leu Ala Ile Gly Ala Ile Phe Ala Ala Thr Asp Ser Val Cys
145 150 155 160

Thr Leu Gln Val Leu Asn Gln Asp Glu Thr Pro Leu Leu Tyr Ser Leu
165 170 175

Val Phe Gly Glu Gly Val Val Asn Asp Ala Thr Ser Val Val Val Phe
180 185 190

Asn Ala Ile Gln Ser Phe Asp Leu Thr His Leu Asn His Glu Ala Ala
195 200 205

Phe His Leu Leu Gly Asn Phe Leu Tyr Leu Phe Leu Leu Ser Thr Leu
210 215 220

Leu Gly Ala Ala Thr Gly Leu Ile Ser Ala Tyr Val Ile Lys Lys Leu
225 230 235 240

Tyr Phe Gly Arg His Ser Thr Asp Arg Glu Val Ala Leu Met Met Leu
245 250 255

Met Ala Tyr Leu Ser Tyr Met Leu Ala Glu Leu Phe Asp Leu Ser Gly
260 265 270

Ile Leu Thr Val Phe Phe Cys Gly Ile Val Met Ser His Tyr Thr Trp
275 280 285

His Asn Val Thr Glu Ser Ser Arg Ile Thr Thr Lys His Thr Phe Ala
290 295 300

Thr Leu Ser Phe Leu Ala Glu Thr Phe Ile Phe Leu Tyr Val Gly Met
305 310 315 320

Asp Ala Leu Asp Ile Asp Lys Trp Arg Ser Val Ser Asp Thr Pro Gly
325 330 335

Thr Ser Ile Ala Val Ser Ser Ile Leu Met Gly Leu Val Met Val Gly
340 345 350

Arg Ala Ala Phe Val Phe Pro Leu Ser Phe Leu Ser Asn Leu Ala Lys
355 360 365

Lys Asn Gln Ser Glu Lys Ile Asn Phe Asn Met Gln Val Val Ile Trp
370 375 380

Trp Ser Gly Leu Met Arg Gly Ala Val Ser Met Ala Leu Ala Tyr Asn
385 390 395 400

Lys Phe Thr Arg Ala Gly His Thr Asp Val Arg Gly Asn Ala Ile Met
405 410 415

Ile Thr Ser Thr Ile Thr Val Cys Leu Phe Ser Thr Val Val Phe Gly
420 425 430

Met Leu Thr Lys Pro Leu Ile Ser Tyr Leu Leu Pro His Gln Asn Ala
435 440 445

Thr Thr Ser Met Leu Ser Asp Asp Asn Thr Pro Lys Ser Ile His Ile
450 455 460

Pro Leu Leu Asp Gln Asp Ser Phe Ile Glu Pro Ser Gly Asn His Asn
465 470 475 480

Val Pro Arg Pro Asp Ser Ile Arg Gly Phe Leu
485 490

<210> 9
<211> 1362
<212> DNA
<213> Artificial

<220>
<223> Modified AtNHX1 DL-3.

<400> 9
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gaagagaata gatggatgaa cgaatccatc accgccttgt tgattggct aggcaactggt 180
gttaccattt tggatttag taaaggaaaa agctcgcatc ttctcgatc tagtgaagat 240

cttttcttca tatactttt gccaccatt atattcaatg cagggttca agtaaaaaag	300
aagcagttt tccgcaattt cgtgactatt atgcttttg gtgctgtgg gactattatt	360
tcttgcacaa tcataatctct aggtgtaaca cagttctta agaagttgga cattggaacc	420
tttgacttgg gtgattatct tgctatttgt gccatatttgc tgcacacaga ttcatatgt	480
acactgcagg ttctgaatca agacgagaca ccttgctt acagtcttgtt attcggagag	540
ggtgttgtga atgatgcaac gtcagttgtg gtcttcaacg cgattcagag ctttgatctc	600
actcaccctaa accacgaagc tgctttcat cttcttgaa acttcttgta tttgtttctc	660
ctaagtacct tgcttggtgc tgcaaccggc ctgataagtgc cgtatgttat caagaagcta	720
tactttggaa ggcactcaac tgaccgagag gttgcctta tgcatttttat ggcgtatctt	780
tcttatatgc ttgctgagct ttgcacttg agcggtatcc tcactgtgtt tttctgttgt	840
attgtatgtt cccattacac atggcacaat gtaacggaga gctcaagaat aacaacaaag	900
catacctttg caactttgtc atttcttgcg gagacatttgc tttcttgta tggtggaaatg	960
gatgccttgg acattgacaa gtggagatcc gtgagtgaca caccggaaac atcgatcgca	1020
gtgagctcaa tcctaattggg tctggcatg gttggaaagag cagcgttcgt cttccgtta	1080
tcgtttctat ctaacttagc caagaagaat caaagcgaga aaatcaactt taacatgcag	1140
gttgtgattt ggtggctgg tctcatgaga ggtgctgtat ctatggctct tgcataacaac	1200
aagtttacaa gggccgggca cacagatgta cgcggaaatg caatcatgat cacgagtacg	1260
ataactgtct gtcttttag cacagtggtg tttggatgc tgaccaaacc actcataaagc	1320
tacctattac cgccaccagaa cgccaccacg agcatgttat ct	1362

<210> 10
 <211> 454
 <212> PRT
 <213> Artificial

<220>
 <223> Putative amino acid encoded by modified AtNHX1 DL-3.

<400> 10

Met	Leu	Asp	Ser	Leu	Val	Ser	Lys	Leu	Pro	Ser	Leu	Ser	Thr	Ser	Asp
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His	Ala	Ser	Val	Val	Ala	Leu	Asn	Leu	Phe	Val	Ala	Leu	Leu	Cys	Ala
			20				25						30		

Cys	Ile	Val	Leu	Gly	His	Leu	Leu	Glu	Glu	Asn	Arg	Trp	Met	Asn	Glu
				35			40			45					

Ser Ile Thr Ala Leu Leu Ile Gly Leu Gly Thr Gly Val Thr Ile Leu
50 55 60

Leu Ile Ser Lys Gly Lys Ser Ser His Leu Leu Val Phe Ser Glu Asp
65 70 75 80

Leu Phe Phe Ile Tyr Leu Leu Pro Pro Ile Ile Phe Asn Ala Gly Phe
85 90 95

Gln Val Lys Lys Lys Gln Phe Phe Arg Asn Phe Val Thr Ile Met Leu
100 105 110

Phe Gly Ala Val Gly Thr Ile Ile Ser Cys Thr Ile Ile Ser Leu Gly
115 120 125

Val Thr Gln Phe Phe Lys Lys Leu Asp Ile Gly Thr Phe Asp Leu Gly
130 135 140

Asp Tyr Leu Ala Ile Gly Ala Ile Phe Ala Ala Thr Asp Ser Val Cys
145 150 155 160

Thr Leu Gln Val Leu Asn Gln Asp Glu Thr Pro Leu Leu Tyr Ser Leu
165 170 175

Val Phe Gly Glu Gly Val Val Asn Asp Ala Thr Ser Val Val Val Phe
180 185 190

Asn Ala Ile Gln Ser Phe Asp Leu Thr His Leu Asn His Glu Ala Ala
195 200 205

Phe His Leu Leu Gly Asn Phe Leu Tyr Leu Phe Leu Leu Ser Thr Leu
210 215 220

Leu Gly Ala Ala Thr Gly Leu Ile Ser Ala Tyr Val Ile Lys Lys Leu
225 230 235 240

Tyr Phe Gly Arg His Ser Thr Asp Arg Glu Val Ala Leu Met Met Leu
245 250 255

Met Ala Tyr Leu Ser Tyr Met Leu Ala Glu Leu Phe Asp Leu Ser Gly
260 265 270

Ile Leu Thr Val Phe Phe Cys Gly Ile Val Met Ser His Tyr Thr Trp
275 280 285

His Asn Val Thr Glu Ser Ser Arg Ile Thr Thr Lys His Thr Phe Ala

290

295

300

Thr Leu Ser Phe Leu Ala Glu Thr Phe Ile Phe Leu Tyr Val Gly Met
305 310 315 320

Asp Ala Leu Asp Ile Asp Lys Trp Arg Ser Val Ser Asp Thr Pro Gly
325 330 335

Thr Ser Ile Ala Val Ser Ser Ile Leu Met Gly Leu Val Met Val Gly
340 345 350

Arg Ala Ala Phe Val Phe Pro Leu Ser Phe Leu Ser Asn Leu Ala Lys
355 360 365

Lys Asn Gln Ser Glu Lys Ile Asn Phe Asn Met Gln Val Val Ile Trp
370 375 380

Trp Ser Gly Leu Met Arg Gly Ala Val Ser Met Ala Leu Ala Tyr Asn
385 390 395 400

Lys Phe Thr Arg Ala Gly His Thr Asp Val Arg Gly Asn Ala Ile Met
405 410 415

Ile Thr Ser Thr Ile Thr Val Cys Leu Phe Ser Thr Val Val Phe Gly
420 425 430

Met Leu Thr Lys Pro Leu Ile Ser Tyr Leu Leu Pro His Gln Asn Ala
435 440 445

Thr Thr Ser Met Leu Ser
450

<210> 11
<211> 1566
<212> DNA
<213> Artificial

<220>
<223> Modified AtNHX1 NDL-1 cDNA.

<400> 11
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ctaggcactg gtgttaccat tttgttgatt agtaaaggaa aaagctcgca tcttctcgtc 180
tttagtgaag atctttctt catatatctt ttgccaccca ttatattcaa tgcagggtt 240
caagtaaaaa agaagcagtt tttccgcaat ttcgtgacta ttatgcttt tggtgctgtt 300

gggactatta	tttcttgcac	aatcatatct	ctaggtgtaa	cacagttctt	taagaagttg	360
gacattggaa	ccttgactt	gggtgattat	cttgctattg	gtgccatatt	tgctgcaaca	420
gattcagttat	gtacactgca	ggttctgaat	caagacgaga	caccttgct	ttacagtctt	480
gtattcggag	agggtgttgt	gaatgatgca	acgtcagttg	tggtcttcaa	cgcgattcag	540
agctttgatc	tcactcacct	aaaccacgaa	gctgctttc	atcttcttgg	aaacttcttg	600
tatttgttcc	tcctaagtag	cttgcttgg	gctgcaaccg	gtctgataag	tgcgtatgtt	660
atcaagaagc	tatactttgg	aaggcactca	actgaccgag	aggttgccct	tatgatgctt	720
atggcgtatc	tttcttata	gcttgctgag	ctttcgact	tgagcggtat	cctcaactgt	780
tttttctgt	gtatttgtat	gtcccattac	acatggcaca	atgtaacgga	gagctcaaga	840
ataacaacaa	agcatacctt	tgcaactttg	tcatttcttgc	cgagagacatt	tatttcttg	900
tatgttggaa	tggatgcctt	ggacatttgac	aagtggagat	ccgtgagtga	cacaccggaa	960
acatcgatcg	cagttagctc	aatcctaattg	ggtctggta	tggttggaag	agcagcgttc	1020
gtctttccgt	tatcgtttct	atctaactta	gccaagaaga	atcaaagcga	gaaaatcaac	1080
tttaacatgc	aggttgtat	ttggtggtct	ggtctcatga	gaggtgctgt	atctatggct	1140
cttgcataca	acaagtttac	aaggccggg	cacacagatg	tacgcgggaa	tgcaatcatg	1200
atcacgagta	cgataactgt	ctgtctttt	agcacagtgg	tgtttggat	gctgaccaaa	1260
ccactcataa	gctacctatt	accgcaccag	aacgccacca	cgagcatgtt	atctgatgac	1320
aacaccccaa	aatccataca	tatccctttg	ttggaccaag	actcgatcat	tgagccttca	1380
gggaaccaca	atgtgcctcg	gcctgacagt	atacggtgt	tcttgacacg	gcccactcga	1440
accgtgcatt	actactggag	acaatttgat	gactccttca	tgcgacccgt	cttggaggt	1500
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aaggct						1566

<210> 12
 <211> 522
 <212> PRT
 <213> Artificial

<220>
 <223> Putative amino acid encoded by modified AtNHX1 NDL-1 cDNA.
 <400> 12

Met Ala Ser Val Val Ala Leu Asn Leu Phe Val Ala Leu Leu Cys Ala
 1 5 10 15

Cys Ile Val Leu Gly His Leu Leu Glu Glu Asn Arg Trp Met Asn Glu

20

25

30

Ser Ile Thr Ala Leu Leu Ile Gly Leu Gly Thr Gly Val Thr Ile Leu
35 40 45

Leu Ile Ser Lys Gly Lys Ser Ser His Leu Leu Val Phe Ser Glu Asp
50 55 60

Leu Phe Phe Ile Tyr Leu Leu Pro Pro Ile Ile Phe Asn Ala Gly Phe
65 70 75 80

Gln Val Lys Lys Lys Gln Phe Phe Arg Asn Phe Val Thr Ile Met Leu
85 90 95

Phe Gly Ala Val Gly Thr Ile Ile Ser Cys Thr Ile Ile Ser Leu Gly
100 105 110

Val Thr Gln Phe Phe Lys Lys Leu Asp Ile Gly Thr Phe Asp Leu Gly
115 120 125

Asp Tyr Leu Ala Ile Gly Ala Ile Phe Ala Ala Thr Asp Ser Val Cys
130 135 140

Thr Leu Gln Val Leu Asn Gln Asp Glu Thr Pro Leu Leu Tyr Ser Leu
145 150 155 160

Val Phe Gly Glu Gly Val Val Asn Asp Ala Thr Ser Val Val Val Phe
165 170 175

Asn Ala Ile Gln Ser Phe Asp Leu Thr His Leu Asn His Glu Ala Ala
180 185 190

Phe His Leu Leu Gly Asn Phe Leu Tyr Leu Phe Leu Leu Ser Thr Leu
195 200 205

Leu Gly Ala Ala Thr Gly Leu Ile Ser Ala Tyr Val Ile Lys Lys Leu
210 215 220

Tyr Phe Gly Arg His Ser Thr Asp Arg Glu Val Ala Leu Met Met Leu
225 230 235 240

Met Ala Tyr Leu Ser Tyr Met Leu Ala Glu Leu Phe Asp Leu Ser Gly
245 250 255

Ile Leu Thr Val Phe Phe Cys Gly Ile Val Met Ser His Tyr Thr Trp
260 265 270

His Asn Val Thr Glu Ser Ser Arg Ile Thr Thr Lys His Thr Phe Ala
275 280 285

Thr Leu Ser Phe Leu Ala Glu Thr Phe Ile Phe Leu Tyr Val Gly Met
290 295 300

Asp Ala Leu Asp Ile Asp Lys Trp Arg Ser Val Ser Asp Thr Pro Gly
305 310 315 320

Thr Ser Ile Ala Val Ser Ser Ile Leu Met Gly Leu Val Met Val Gly
325 330 335

Arg Ala Ala Phe Val Phe Pro Leu Ser Phe Leu Ser Asn Leu Ala Lys
340 345 350

Lys Asn Gln Ser Glu Lys Ile Asn Phe Asn Met Gln Val Val Ile Trp
355 360 365

Trp Ser Gly Leu Met Arg Gly Ala Val Ser Met Ala Leu Ala Tyr Asn
370 375 380

Lys Phe Thr Arg Ala Gly His Thr Asp Val Arg Gly Asn Ala Ile Met
385 390 395 400

Ile Thr Ser Thr Ile Thr Val Cys Leu Phe Ser Thr Val Val Phe Gly
405 410 415

Met Leu Thr Lys Pro Leu Ile Ser Tyr Leu Leu Pro His Gln Asn Ala
420 425 430

Thr Thr Ser Met Leu Ser Asp Asp Asn Thr Pro Lys Ser Ile His Ile
435 440 445

Pro Leu Leu Asp Gln Asp Ser Phe Ile Glu Pro Ser Gly Asn His Asn
450 455 460

Val Pro Arg Pro Asp Ser Ile Arg Gly Phe Leu Thr Arg Pro Thr Arg
465 470 475 480

Thr Val His Tyr Tyr Trp Arg Gln Phe Asp Asp Ser Phe Met Arg Pro
485 490 495

Val Phe Gly Gly Arg Gly Phe Val Pro Phe Val Pro Gly Ser Pro Thr
500 505 510

Glu Arg Asn Pro Pro Asp Leu Ser Lys Ala
515 520

<210> 13
<211> 1410
<212> DNA
<213> Artificial

<220>
<223> NDL-2 cDNA.

<400> 13
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actattatgc tttttgggtgc tggggactt attatttctt gcacaatcat atctctaggt 180
gtaacacagt tcttaagaa gttggacatt ggaaccttg acttgggtga ttatcttgct 240
attggtgcca tatttgctgc aacagattca gtatgtacac tgcagggtct gaatcaagac 300
gagacacctt tgctttacag tcttgatttgc ggagagggtg ttgtgaatga tgcaacgtca 360
gttgggtct tcaacgcgat tcagagcttt gatctcactc acctaaacca cgaagctgct 420
tttcatcttc ttggaaactt cttgtatttgc tttctcctaa gtaccttgct ttgtgctgca 480
accggctctga taagtgcgta tggatcaag aagctatact ttggaaggca ctcaactgac 540
cgagagggttgc cccttatgtat gcttatggcg tatctttctt atatgcttgc tgagctttc 600
gacttgagcg gtatcctcac tggatggatc tgggttgc tggatgtccca ttacacatgg 660
cacaatgtaa cggagagctc aagaataaca acaaagcata ccttgcaac ttgtcattt 720
cttgcggaga catttatttt cttgtatgtt ggaatggatc cttggacat tgacaagtgg 780
agatccgtga gtgacacacc gggAACATCG atcgcagtga gctcaatcct aatgggtctg 840
gtcatgggttgc gaagagcagc gttcgtctt ccgttatcgt ttctatctaa cttagccaa 900
aagaatcaaa gcgagaaaat caacttaac atgcagggttgc tgatgggtgc gtctggtctc 960
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caagactcgt tcattgagcc ttcaggaaac cacaatgtgc ctcggcctga cagtatacgt 1260
ggcttcttgc cacggccac tcgaaccgttgc cattactact ggagacaatt tgatgactcc 1320
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gagagaaacc ctcctgatct tagtaaggct 1410

<210> 14
<211> 470
<212> PRT
<213> Artificial

<220>
<223> Putative amino acid encoded by modified AtNHX1 NDL-2 cDNA.

<400> 14

Met Lys Ser Ser His Leu Leu Val Phe Ser Glu Asp Leu Phe Phe Ile
1 5 10 15

Tyr Leu Leu Pro Pro Ile Ile Phe Asn Ala Gly Phe Gln Val Lys Lys
20 25 30

Lys Gln Phe Phe Arg Asn Phe Val Thr Ile Met Leu Phe Gly Ala Val
35 40 45

Gly Thr Ile Ile Ser Cys Thr Ile Ile Ser Leu Gly Val Thr Gln Phe
50 55 60

Phe Lys Lys Leu Asp Ile Gly Thr Phe Asp Leu Gly Asp Tyr Leu Ala
65 70 75 80

Ile Gly Ala Ile Phe Ala Ala Thr Asp Ser Val Cys Thr Leu Gln Val
85 90 95

Leu Asn Gln Asp Glu Thr Pro Leu Leu Tyr Ser Leu Val Phe Gly Glu
100 105 110

Gly Val Val Asn Asp Ala Thr Ser Val Val Val Phe Asn Ala Ile Gln
115 120 125

Ser Phe Asp Leu Thr His Leu Asn His Glu Ala Ala Phe His Leu Leu
130 135 140

Gly Asn Phe Leu Tyr Leu Phe Leu Leu Ser Thr Leu Leu Gly Ala Ala
145 150 155 160

Thr Gly Leu Ile Ser Ala Tyr Val Ile Lys Lys Leu Tyr Phe Gly Arg
165 170 175

His Ser Thr Asp Arg Glu Val Ala Leu Met Met Leu Met Ala Tyr Leu
180 185 190

Ser Tyr Met Leu Ala Glu Leu Phe Asp Leu Ser Gly Ile Leu Thr Val

195

200

205

Phe Phe Cys Gly Ile Val Met Ser His Tyr Thr Trp His Asn Val Thr
210 215 220

Glu Ser Ser Arg Ile Thr Thr Lys His Thr Phe Ala Thr Leu Ser Phe
225 230 235 240

Leu Ala Glu Thr Phe Ile Phe Leu Tyr Val Gly Met Asp Ala Leu Asp
245 250 255

Ile Asp Lys Trp Arg Ser Val Ser Asp Thr Pro Gly Thr Ser Ile Ala
260 265 270

Val Ser Ser Ile Leu Met Gly Leu Val Met Val Gly Arg Ala Ala Phe
275 280 285

Val Phe Pro Leu Ser Phe Leu Ser Asn Leu Ala Lys Lys Asn Gln Ser
290 295 300

Glu Lys Ile Asn Phe Asn Met Gln Val Val Ile Trp Trp Ser Gly Leu
305 310 315 320

Met Arg Gly Ala Val Ser Met Ala Leu Ala Tyr Asn Lys Phe Thr Arg
325 330 335

Ala Gly His Thr Asp Val Arg Gly Asn Ala Ile Met Ile Thr Ser Thr
340 345 350

Ile Thr Val Cys Leu Phe Ser Thr Val Val Phe Gly Met Leu Thr Lys
355 360 365

Pro Leu Ile Ser Tyr Leu Leu Pro His Gln Asn Ala Thr Thr Ser Met
370 375 380

Leu Ser Asp Asp Asn Thr Pro Lys Ser Ile His Ile Pro Leu Leu Asp
385 390 395 400

Gln Asp Ser Phe Ile Glu Pro Ser Gly Asn His Asn Val Pro Arg Pro
405 410 415

Asp Ser Ile Arg Gly Phe Leu Thr Arg Pro Thr Arg Thr Val His Tyr
420 425 430

Tyr Trp Arg Gln Phe Asp Asp Ser Phe Met Arg Pro Val Phe Gly Gly
435 440 445

Arg Gly Phe Val Pro Phe Val Pro Gly Ser Pro Thr Glu Arg Asn Pro
450 455 460

Pro Asp Leu Ser Lys Ala
465 470

<210> 15
<211> 1323
<212> DNA
<213> Artificial

<220>
<223> NDL-3 cDNA.

<400> 15
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attggAACCT ttgacttggg tgattatctt gctattggg ccatatttgc tgcaacagat 180
tcaGtatgtt cactgcagg tctgaatcaa gacgagacac ctttgctta cagtcttgc 240
ttcggagagg gtgttgtgaa tgatgcaacg tcagttgtgg tcttcaacgc gattcagagc 300
tttgatctca ctcacctaataa ccacgaagct gctttcato ttcttgaaa cttcttgc 360
ttgtttctcc taagtacctt gcttgggct gcaaccggc tgataagtgc gtatgttac 420
aagaagctat acttttggaa gcaactcaact gaccgagagg ttgcccttat gatgcttatg 480
gcgtatcttt cttatatgct tgctgagctt ttcgacttga gcggtatcct cactgtgtt 540
ttctgtggta ttgtgatgtc ccattacaca tggcacaatg taacggagag ctcagaata 600
acaacaaagc atacccttgc aactttgtca tttcttgcgg agacatttat tttcttgc 660
gttggaatgg atgccttggc cattgacaag tggagatccg tgagtgacac accggaaaca 720
tcgatcgca g tgagctcaat cctaattgggt ctggcatgg ttggaaagagc agcggtcg 780
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aacatgcagg ttgtgatttg gtggctggg ctcatgagag gtgctgtatc tatggcttt 900
gcataacaaca agtttacaag ggccgggcac acagatgtac gcggaatgc aatcatgatc 960
acgagttacga taactgtctg tcttttagc acagtgggtgt ttggatgtc gaccaaaacca 1020
ctcataagct acctattacc gcaccagaac gccaccacga gcatgttac tgatgacaac 1080
accccaaaat ccatacatat ccctttgtt gaccaagact cggtcattga gccttcagg 1140
aaccacaatg tgcctcggcc tgacagtata cgtggcttct tgacacggcc cactcgaacc 1200
gtgcattact actggagaca atttgatgac tccttcattgc gacccgtctt tggaggtcgt 1260

ggctttgtac cctttgttcc aggttctcca actgagagaa accctcctga tcttagtaag 1320
gct 1323

<210> 16
<211> 439
<212> PRT
<213> Artificial

<220>
<223> Putative amino acid encoded by modified AtNHX1 NDL-3 cDNA.

<400> 16

Met Lys Lys Lys Gln Phe Phe Arg Asn Phe Val Thr Ile Met Leu Phe
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Gly Ala Val Gly Thr Ile Ile Ser Cys Thr Ile Ile Ser Leu Gly Val
20 25 30

Thr Gln Phe Phe Lys Lys Leu Asp Ile Gly Thr Phe Asp Leu Gly Asp
35 40 45

Tyr Leu Ala Ile Gly Ala Ile Phe Ala Ala Thr Asp Ser Val Cys Thr
50 55 60

Leu Gln Val Leu Asn Gln Asp Glu Thr Pro Leu Leu Tyr Ser Leu Val
65 70 75 80

Phe Gly Glu Gly Val Val Asn Asp Ala Thr Ser Trp Val Phe Asn Ala
85 90 95

Ile Gln Ser Phe Asp Leu Thr His Leu Asn His Glu Ala Ala Phe His
100 105 110

Leu Leu Gly Asn Phe Leu Tyr Leu Phe Leu Leu Ser Thr Leu Leu Gly
115 120 125

Ala Ala Thr Gly Leu Ile Ser Ala Tyr Val Ile Lys Lys Leu Tyr Phe
130 135 140

Gly Arg His Ser Thr Asp Arg Glu Val Ala Leu Met Met Leu Met Ala
145 150 155 160

Tyr Leu Ser Tyr Met Leu Ala Glu Leu Phe Asp Leu Ser Gly Ile Leu
165 170 175

Thr Val Phe Phe Cys Gly Ile Val Met Ser His Tyr Thr Trp His Asn
180 185 190

Val Thr Glu Ser Ser Arg Ile Thr Thr Lys His Thr Phe Ala Thr Leu
195 200 205

Ser Phe Leu Ala Glu Thr Phe Ile Phe Leu Tyr Val Gly Met Asp Ala
210 215 220

Leu Asp Ile Asp Lys Trp Arg Ser Val Ser Asp Thr Pro Gly Thr Ser
225 230 235 240

Ile Ala Val Ser Ser Ile Leu Met Gly Leu Val Met Val Gly Arg Ala
245 250 255

Ala Phe Val Phe Pro Leu Ser Phe Leu Ser Asn Leu Ala Lys Lys Asn
260 265 270

Gln Ser Glu Lys Ile Asn Phe Asn Met Gln Trp Ile Trp Trp Ser Gly
275 280 285

Leu Met Arg Gly Ala Val Ser Met Ala Leu Ala Tyr Asn Lys Phe Thr
290 295 300

Arg Ala Gly His Thr Asp Val Arg Gly Asn Ala Ile Met Ile Thr Ser
305 310 315 320

Thr Ile Thr Val Cys Leu Phe Ser Thr Val Val Phe Gly Met Leu Thr
325 330 335

Lys Pro Leu Ile Ser Tyr Leu Leu Pro His Gln Asn Ala Thr Thr Ser
340 345 350

Met Leu Ser Asp Asp Asn Thr Pro Lys Ser Ile His Ile Pro Leu Leu
355 360 365

Asp Gln Asp Ser Phe Ile Glu Pro Ser Gly Asn His Asn Val Pro Arg
370 375 380

Pro Asp Ser Ile Arg Gly Phe Leu Thr Arg Pro Thr Arg Thr Val His
385 390 395 400

Tyr Tyr Trp Arg Gln Phe Asp Asp Ser Phe Met Arg Pro Val Phe Gly
405 410 415

Gly Arg Gly Phe Val Pro Phe Val Pro Gly Ser Pro Thr Glu Arg Asn
420 425 430

Pro Pro Asp Leu Ser Lys Ala
435

<210> 17
<211> 35
<212> DNA
<213> Artificial

<220>
<223> Putative amino acid encoded by modified AtNHX1 NDL-3 cDNA.

<400> 17
ggagacaatt tgatgactgc ttcatgcgac ccgtc 35

<210> 18
<211> 35
<212> DNA
<213> Artificial

<220>
<223> Primer SM-23-R

<400> 18
gacgggtcgc atgaaggagt catcaaattt tctcc 35

<210> 19
<211> 38
<212> DNA
<213> Artificial

<220>
<223> Primer EXCH-5

<400> 19
agcttaggatc cggatctaga agaagataac aatgttgg 38

<210> 20
<211> 33
<212> DNA
<213> Artificial

<220>
<223> Primer EXCH-DL-1

<400> 20
agctgaattc ctagggtaca aagccacgac ctc 33

<210> 21
<211> 32
<212> DNA
<213> Artificial

<220>
<223> Primer EXCH-DL-2

<400> 21
agctgaattc ctacaagaag ccacgtatac tg

32

<210> 22
<211> 32
<212> DNA
<213> Artificial

<220>
<223> Primer EXCH-DL-3

<400> 22
agctgaattc ctaagataac atgctcggtgg tg

32